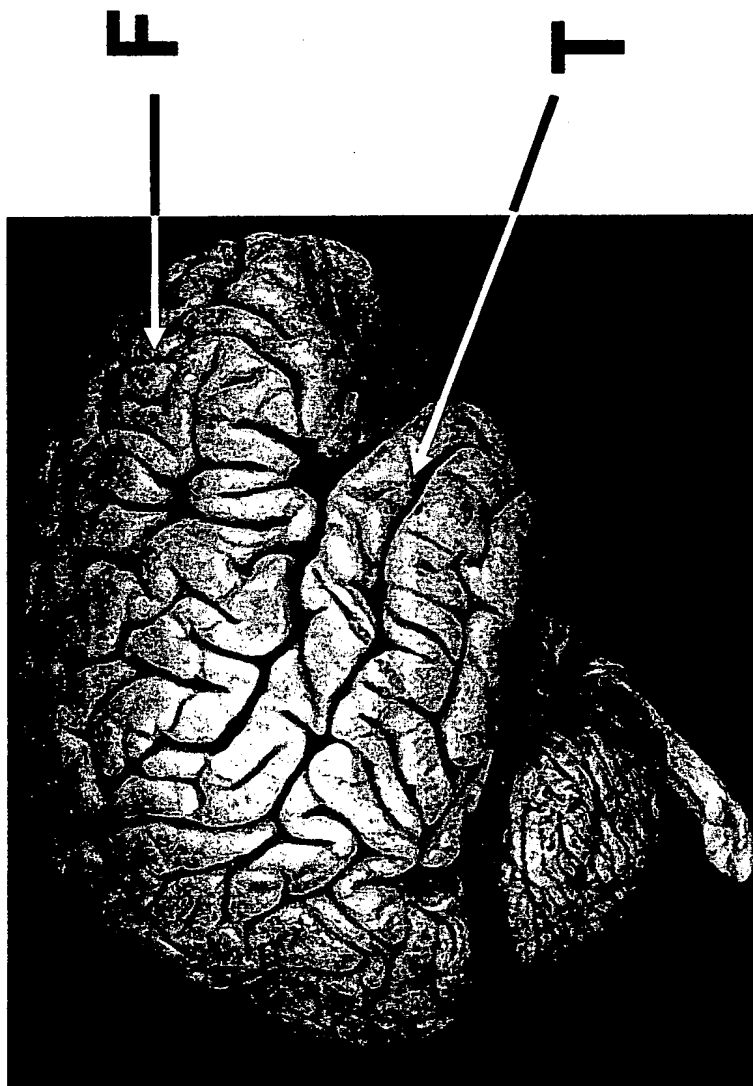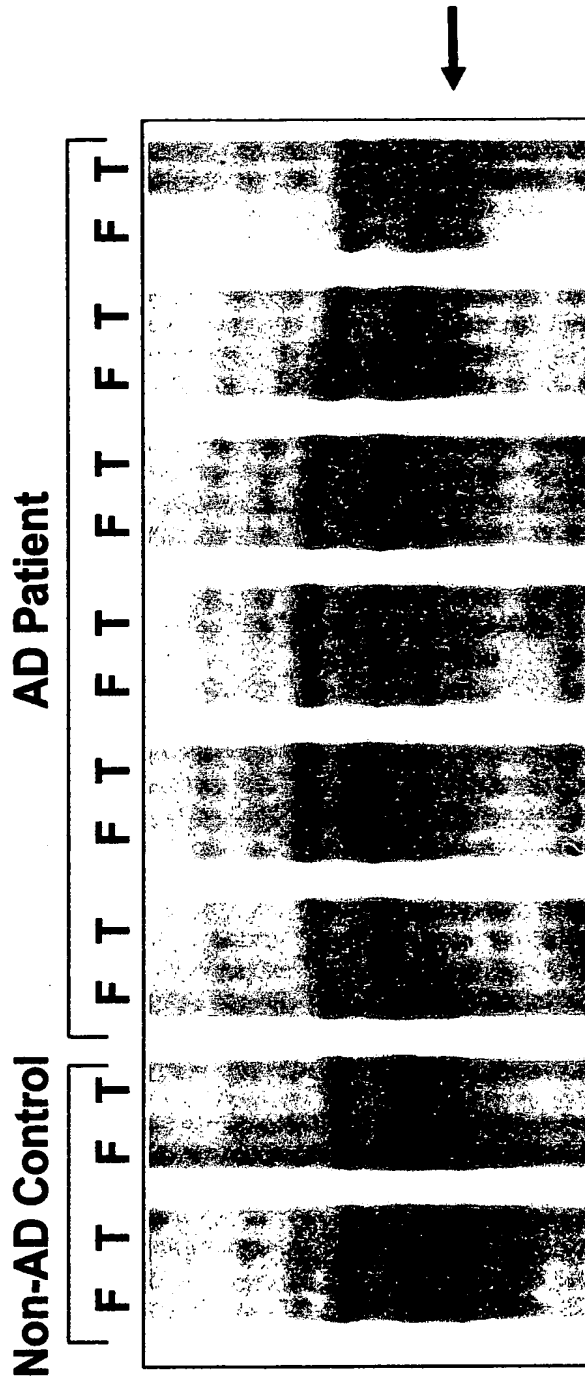Fig. 1: Identification of Genes Involved in Alzheimer's Disease Pathology
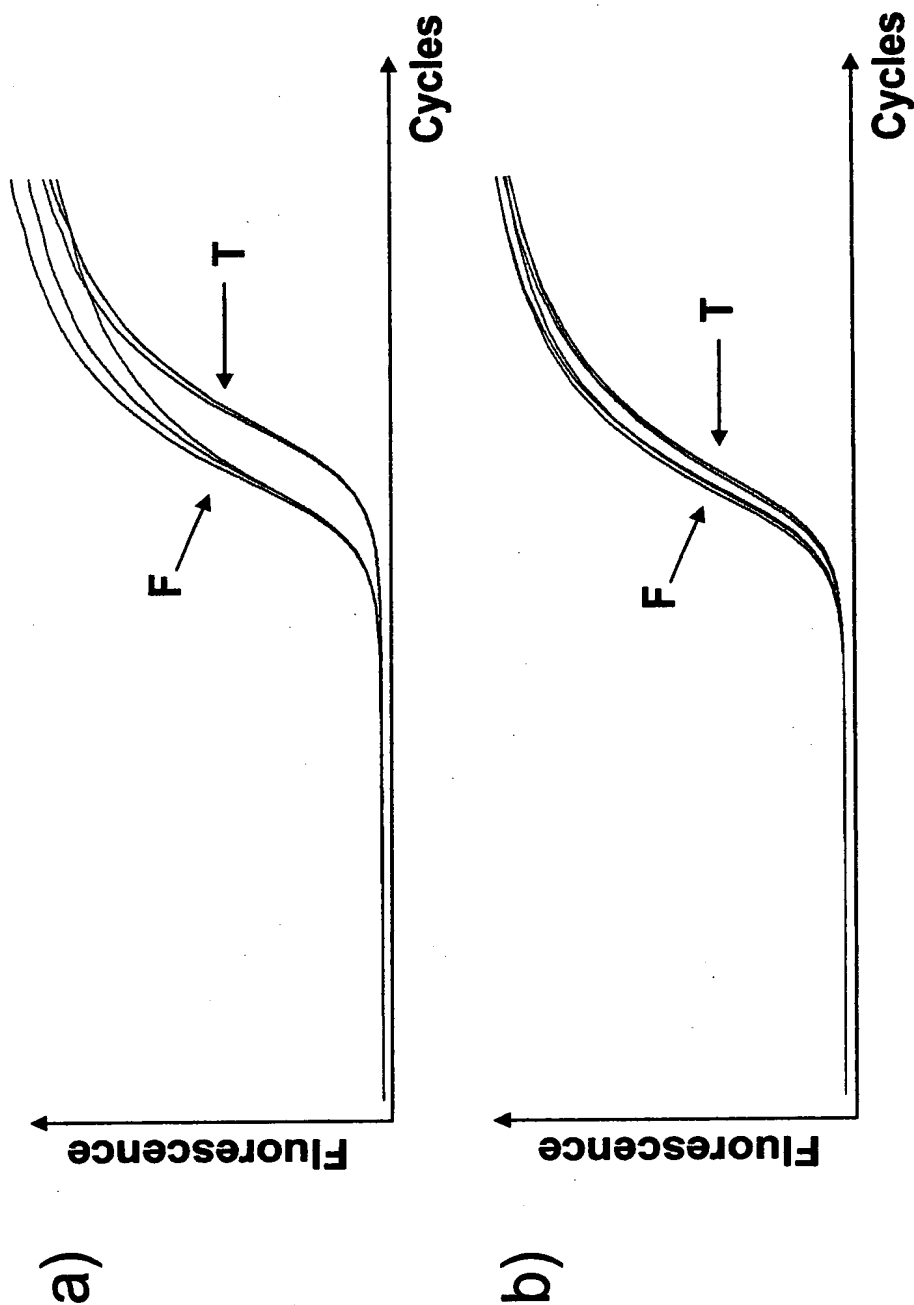
Fig. 2: Identification of differentially expressed genes in a fluorescence differential display screen

Fig. 3: Verification of differential expression of human MAGUIN-1 by quantitative RT-PCR

10/508343

Fig. 4: Verification of differential expression of Maguin-1 by quantitative RT-PCR
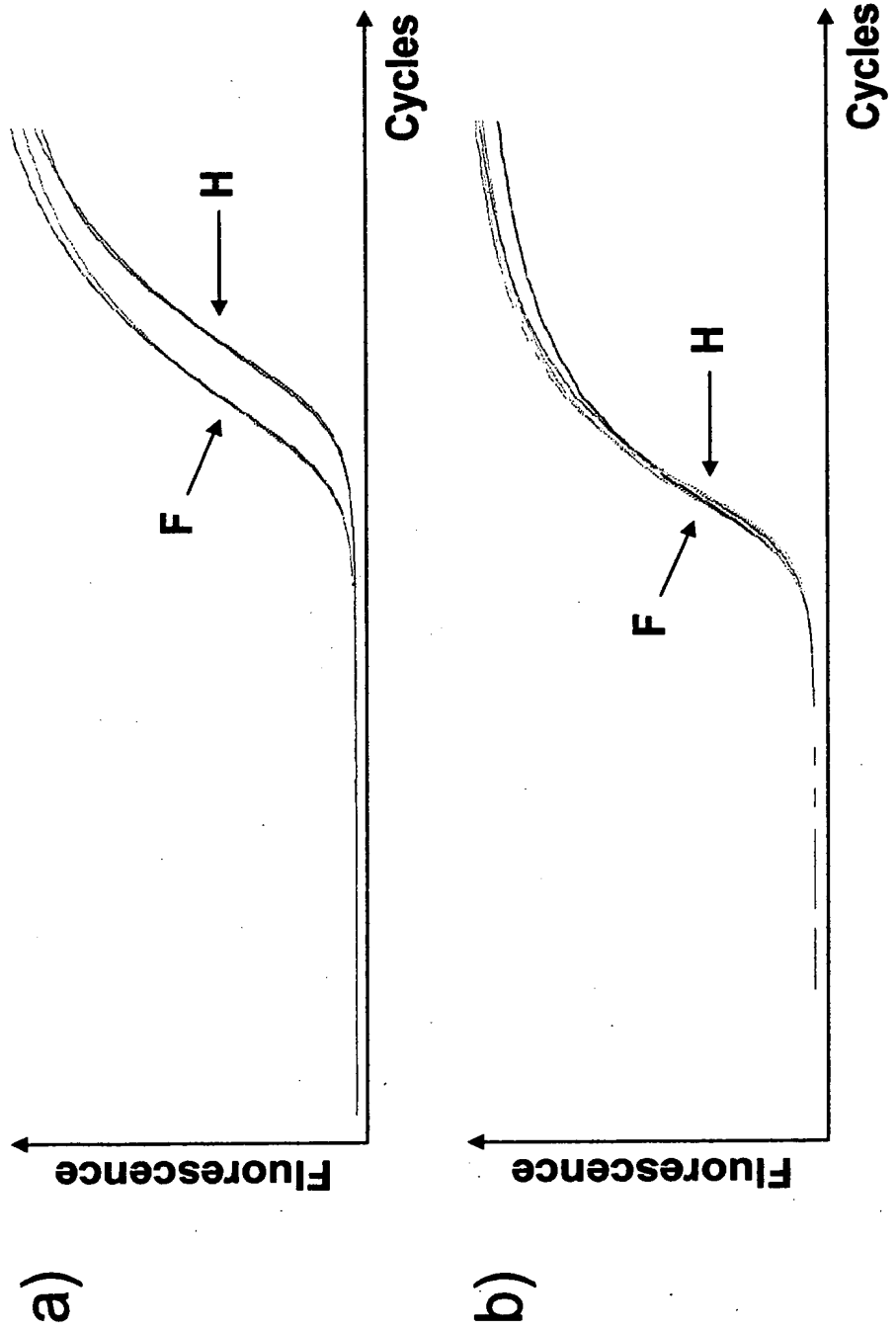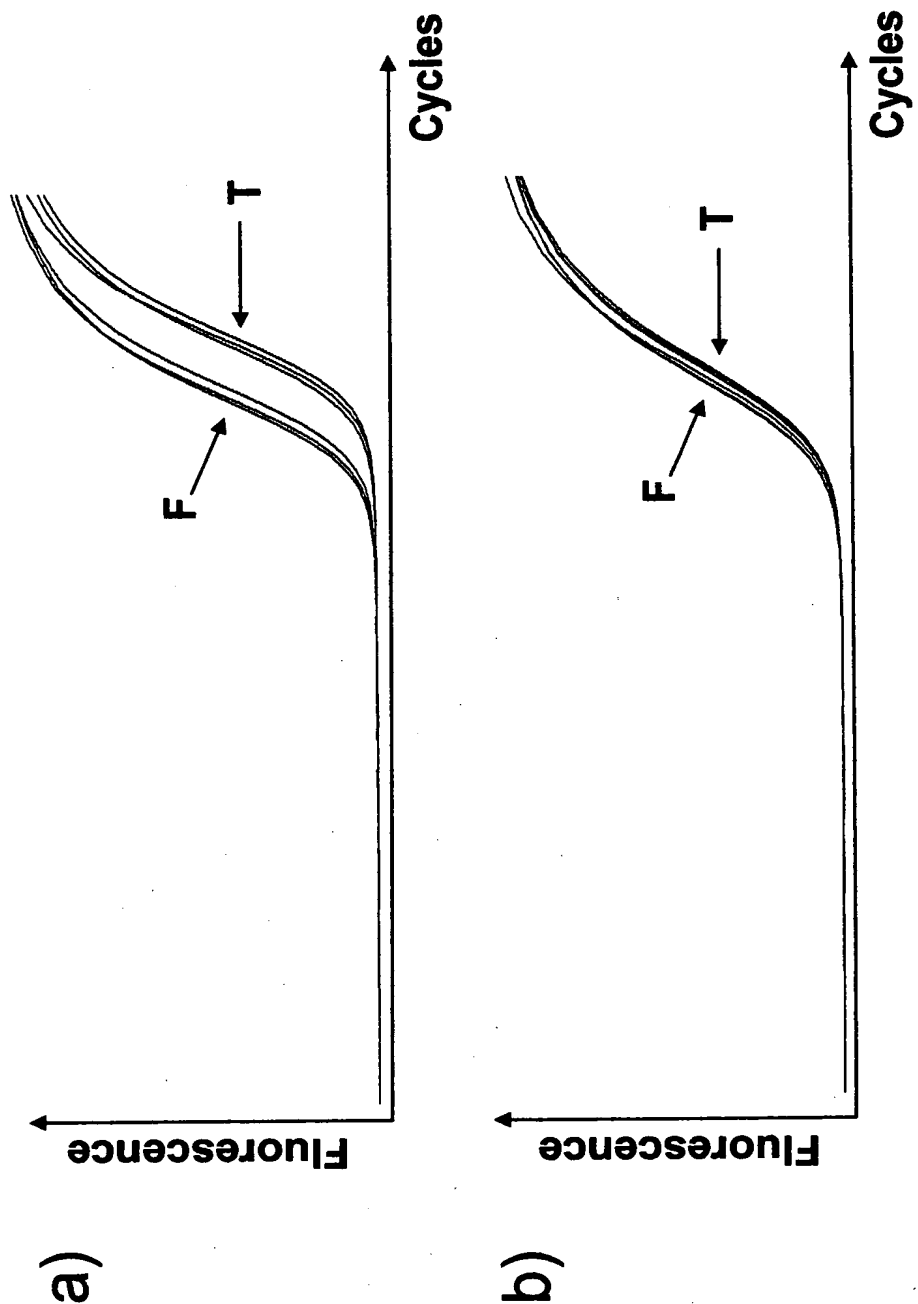
Fig. 5: Verification of differential expression of human MAGUIN-2 by quantitative RT-PCR

Fig. 6: Verification of differential expression of Maguin-2 by quantitative RT-PCR

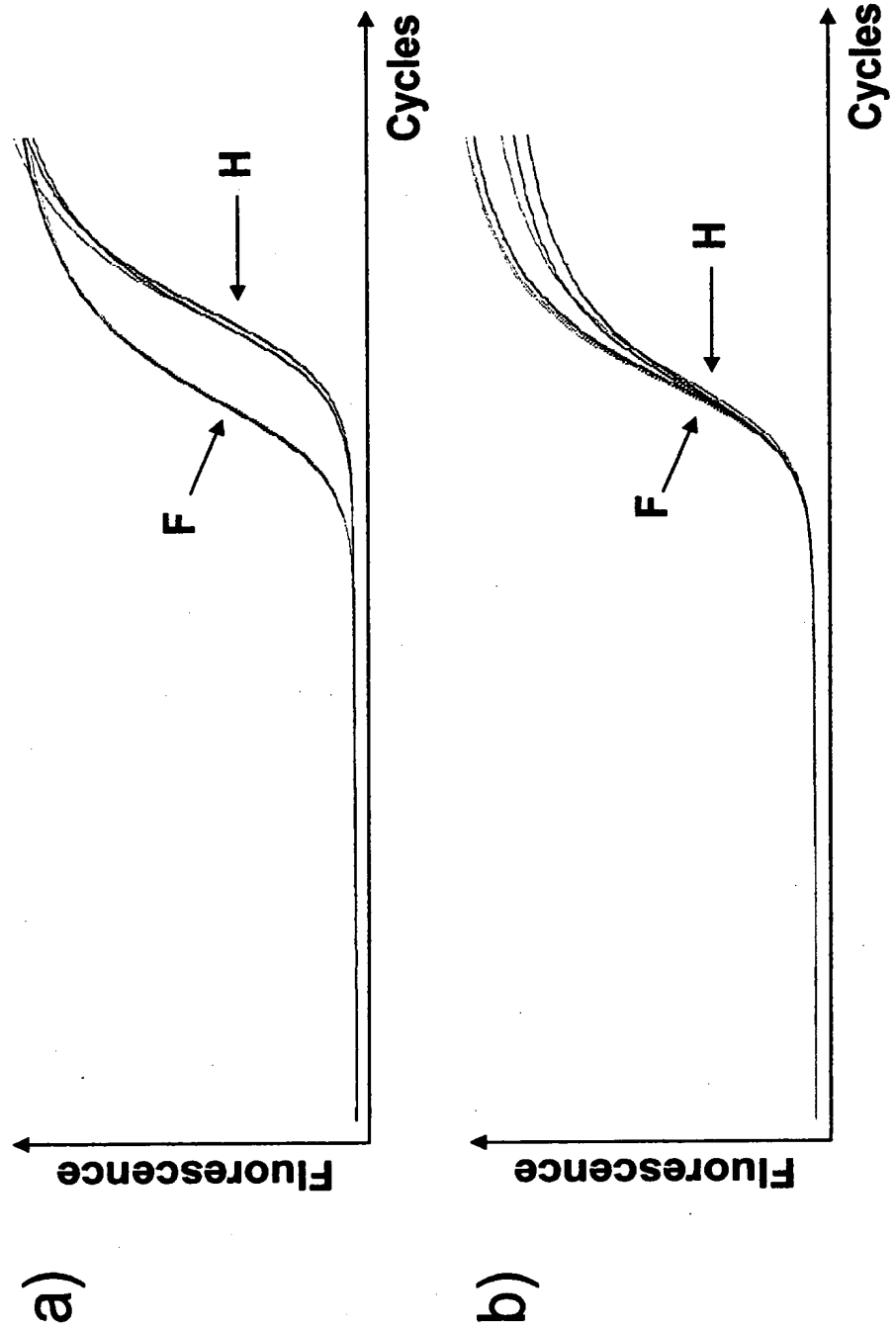# Fig. 7: SEQ ID NO. 1:
amino acid sequence of human MAGUIN-1 protein

Length: 1034 aa

```
   1 MALIMEPVSK WSPSQVVDWM KGLDDCLQQY IKNFEREKIS GDQLLRITHQ

  51 ELEDLGVSRI GHQELILEAV DLLCALNYGL ETENLKTLSH KLNASAKNLQ

 101 NFITGRRRSG HYDGRTSRKL PNDFLTSVVD LIGAAKSLLA WLDRSPFAAV

 151 TDYSVTRNNV IQLCLELTTI VQQDCTVYET ENKILHVCKT LSGVCDHIIS

 201 LSSDPLVSQS AHLEVIQLAN IKPSEGLGMY IKSTYDGLHV ITGTTENSPA

 251 DRCKKIHAGD EVIQVNHQTV VGWQLKNLVN ALREDPSGVI LTLKKRPQSM

 301 LTSAPALLKN MRWKPLALQP LIPRSPTSSV ATPSSTISTP TKRDSSALQD

 351 LYIPPPPAEP YIPRDEKGNL PCEDLRGHMV GKPVHKGSES PNSFLDQEYR

 401 KRFNIVEEDT VLYCYEYEKG RSSSQGRRES TPTYGKLRPI SMPVEYNWVG

 451 DYEDPNKMKR DSRRENSLLR YMSNEKIAQE EYMFQRNSKK DTGKKSKKKG

 501 DKSNSPTHYS LLPSLQMDAL RQDIMGTPVP ETTLYHTFQQ SSLQHKSKKK

 551 NKGPIAGKSK RRISCKDLGR GDCEGWLWKK KDAKSYFSQK WKKYWFVLKD

 601 ASLYWYINEE DEKAEGFISL PEFKIDRASE CRKKYAFKAC HPKIKSFYFA

 651 AEHLDDMNRW LNRINMLTAG YAERERIKQE QDYWSESDKE EADTPSTPKQ

 701 DSPPPPYDTY PRPPSMSCAS PYVEAKHSRL SSTETSQSQS SHEEFRQEVT

 751 GSSAVSPIRK TASQRRSWQD LIETPLTSSG LHYLQTLPLE DSVFSDSAAI

 801 SPEHRRQSTL PTQKCHLQDH YGPYPLAESE RMQVLNGNGG KPRSFTLPRD

 851 SGFNHCCLNA PVSACDPQDD VQPPEVEEEE EEEEEGEAA GENIGEKSES

 901 REEKLGDSLQ DLYRALEQAS LSPLGEHRIS TKMEYKLSFI KRCNDPVMNE

 951 KLHRLRILKS TLKAREGEVA IIDKVLDNPD LTSKEFQQWK QMYLDLFLDI

1001 CQNTTSNDPL SISSEVDVIT SSLAHTHSYI ETHV*
```

Fig. 8: Alignment of SEQ ID NO. 1, human MAGUIN-1, with rat MAGUIN-1

Length: 1034 aa

```
  1 MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ  50
    |||||||||||||||||||||||||||||||||||||||||||||||||
  1 MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ  50

 51 ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ 100
    |||||||||||||||||||||||||||||||||||||||||||||||||
 51 ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ 100

101 NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV 150
    |||||||||||||||||||||||||||||||||||||||||||||||||
101 NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV 150

151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS 200
    |||||||||||||||||||||||||||||||||||||||||||||||||
151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS 200

201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA 250
    |||||||||||||||||||||||||||||||||||||||||||||||||
201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA 250

251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM 300
    |||||||||||||||||||||||||||||||||||||||||||||||||
251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM 300

301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD 350
    |||||||||||||||||||||||||||||||||||||||||||||||||
301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD 350

351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR 400
    |||||||||||||||||||||||||||||||||||||||||||||||||
351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR 400

401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG 450
    |||||||||||||||||||||||||||||||||||||||||||||||||
401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG 450

451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKG 500
    |||||||||||||||||||||||||||||||||||||||||||||||||
451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKG 500
```

```
501 DKSNSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550
    |||:||||||||||||||||||||||||||||||||||||||||||||||
501 DKSTSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550

551 NKGPIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD 600
    |||:||||||||||||||||||||||||||||||||||||||||||||||
551 NKGAIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD 600

601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650

651 AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700
    ||||||||||||||||||||||||||||||||||||||||||||||||||
651 AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700

701 DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT 750
    ||||||||||||||||||||||||||||||||||||||||||||||||||
701 DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT 750

751 GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI 800

801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD 850
    ||||||||||||||||||||||||||||||||||||||||||||||||||
801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD 850

851 SGFNHCCLNAPVSACDPQDDVQPPEVEEEEEEEEEGEAAGENIGEKSES 900
    |||||||||||||||||||||||:|||||||||||||   ||||||||||:|:
851 SGFNHCCLNAPVSACDPQDDIQPPEVEEEEEEEE..EAAGENIGEKNEN 898

901 REEKLGDSLQDLYRALEQASLSPLGEHRISTKMEYKLSFIKRCNDPVMNE 950
    ||||||||||||||||:|||||||||||||||:|||||||||||||||||
899 REEKLGDSLQDLYRALEEASLSPLGEHRISTKIEYKLSFIKRCNDPVMNE 948

951 KLHRLRILKSTLKAREGEVAIIDKVLDNPDLTSKEFQQWKQMYLDLFLDI 1000
    ||||||||||||||||||||||||||||||||||||||||||||||||||
949 KLHRLRILKSTLKAREGEVAIIDKVLDNPDLTSKEFQQWKQMYLDLFLDI 998

1001 CQNTTSNDPLSISSEVDVITSSLAHTHSYIETHV 1034
     |||||||||||||||||||||||||:||||||||
999 CQNTTSNDPLSISSEVDVITSSLTHTHSYIETHV 1032
```

Fig. 9: SEQ ID NO. 2: amino acid sequence of human MAGUIN-2 protein

Length: 898 aa

```
  1 MALIMEPVSK WSPSQVVDWM KGLDDCLQQY IKNFEREKIS GDQLLRITHQ

 51 ELEDLGVSRI GHQELILEAV DLLCALNYGL ETENLKTLSH KLNASAKNLQ

101 NFITGRRRSG HYDGRTSRKL PNDFLTSVVD LIGAAKSLLA WLDRSPFAAV

151 TDYSVTRNNV IQLCLELTTI VQQDCTVYET ENKILHVCKT LSGVCDHIIS

201 LSSDPLVSQS AHLEVIQLAN IKPSEGLGMY IKSTYDGLHV ITGTTENSPA

251 DRCKKIHAGD EVIQVNHQTV VGWQLKNLVN ALREDPSGVI LTLKKRPQSM

301 LTSAPALLKN MRWKPLALQP LIPRSPTSSV ATPSSTISTP TKRDSSALQD

351 LYIPPPPAEP YIPRDEKGNL PCEDLRGHMV GKPVHKGSES PNSFLDQEYR

401 KRFNIVEEDT VLYCYEYEKG RSSSQGRRES TPTYGKLRPI SMPVEYNWVG

451 DYEDPNKMKR DSRRENSLLR YMSNEKIAQE EYMFQRNSKK DTGKKSKKKG

501 DKSNSPTHYS LLPSLQMDAL RQDIMGTPVP ETTLYHTFQQ SSLQHKSKKK

551 NKGPIAGKSK RRISCKDLGR GDCEGWLWKK KDAKSYFSQK WKKYWFVLKD

601 ASLYWYINEE DEKAEGFISL PEFKIDRASE CRKKYAFKAC HPKIKSFYFA

651 AEHLDDMNRW LNRINMLTAG YAERERIKQE QDYWSESDKE EADTPSTPKQ

701 DSPPPPYDTY PRPPSMSCAS PYVEAKHSRL SSTETSQSQS SHEEFRQEVT

751 GSSAVSPIRK TASQRRSWQD LIETPLTSSG LHYLQTLPLE DSVFSDSAAI

801 SPEHRRQSTL PTQKCHLQDH YGPYPLAESE RMQVLNGNGG KPRSFTLPRD

851 SGFNHCCLNA PVSACDPQDD VQPPEVEEEE EEEEEGEAA GENIGEKS*
```

Figure 10: Alignment of SEQ ID NO. 2, human MAGUIN-2, with rat MAGUIN-2

Length: 898 aa

```
  1 MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ  50
    |||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MALIMEPVSKWSPSQVVDWMKGLDDCLQQYIKNFEREKISGDQLLRITHQ  50

 51 ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ 100
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 51 ELEDLGVSRIGHQELILEAVDLLCALNYGLETENLKTLSHKLNASAKNLQ 100

101 NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV 150
    |||||||||||||||||||||||||||||||||||||||||||||||||||
101 NFITGRRRSGHYDGRTSRKLPNDFLTSVVDLIGAAKSLLAWLDRSPFAAV 150

151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS 200
    |||||||||||||||||||||||||||||||||||||||||||||||||||
151 TDYSVTRNNVIQLCLELTTIVQQDCTVYETENKILHVCKTLSGVCDHIIS 200

201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA 250
    |||||||||||||||||||||||||||||||||||||||||||||||||||
201 LSSDPLVSQSAHLEVIQLANIKPSEGLGMYIKSTYDGLHVITGTTENSPA 250

251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM 300
    |||||||||||||||||||||||||||||||||||||||||||||||||||
251 DRCKKIHAGDEVIQVNHQTVVGWQLKNLVNALREDPSGVILTLKKRPQSM 300

301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD 350
    |||||||||||||||||||||||||||||||||||||||||||||||||||
301 LTSAPALLKNMRWKPLALQPLIPRSPTSSVATPSSTISTPTKRDSSALQD 350

351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR 400
    |||||||||||||||||||||||||||||||||||||||||||||||||||
351 LYIPPPPAEPYIPRDEKGNLPCEDLRGHMVGKPVHKGSESPNSFLDQEYR 400

401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG 450
    |||||||||||||||||||||||||||||||||||||||||||||||||||
401 KRFNIVEEDTVLYCYEYEKGRSSSQGRRESTPTYGKLRPISMPVEYNWVG 450

451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKG 500
    |||||||||||||||||||||||||||||||||||||||||||||||||||
451 DYEDPNKMKRDSRRENSLLRYMSNEKIAQEEYMFQRNSKKDTGKKSKKKG 500
```

```
501 DKSNSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550
    |||:||||||||||||||||||||||||||||||||||||||||||||||
501 DKSTSPTHYSLLPSLQMDALRQDIMGTPVPETTLYHTFQQSSLQHKSKKK 550

551 NKGPIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD 600
    |||:||||||||||||||||||||||||||||||||||||||||||||||
551 NKGAIAGKSKRRISCKDLGRGDCEGWLWKKKDAKSYFSQKWKKYWFVLKD 600

601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650
    ||||||||||||||||||||||||||||||||||||||||||||||||||
601 ASLYWYINEEDEKAEGFISLPEFKIDRASECRKKYAFKACHPKIKSFYFA 650

651 AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700
    ||||||||||||||||||||||||||||||||||||||||||||||||||
651 AEHLDDMNRWLNRINMLTAGYAERERIKQEQDYWSESDKEEADTPSTPKQ 700

701 DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT 750
    ||||||||||||||||||||||||||||||||||||||||||||||||||
701 DSPPPPYDTYPRPPSMSCASPYVEAKHSRLSSTETSQSQSSHEEFRQEVT 750

751 GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI 800
    ||||||||||||||||||||||||||||||||||||||||||||||||||
751 GSSAVSPIRKTASQRRSWQDLIETPLTSSGLHYLQTLPLEDSVFSDSAAI 800

801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD 850
    ||||||||||||||||||||||||||||||||||||||||||||||||||
801 SPEHRRQSTLPTQKCHLQDHYGPYPLAESERMQVLNGNGGKPRSFTLPRD 850

851 SGFNHCCLNAPVSACDPQDDVQPPEVEEEEEEEEEGEAAGENIGEKS 898
    |||||||||||||||||||||||:|||||||||||||||   |||||||||||
851 SGFNHCCLNAPVSACDPQDDIQPPEVEEEEEEEE..EAAGENIGEKS 896
```

Fig. 11: SEQ ID NO. 3: nucleotide sequence of human MAGUIN-1 coding sequence

Length: 3105 bp

```
   1 ATGGCTCTGA TAATGGAACC GGTGAGCAAA TGGTCTCCGA GTCAAGTAGT GGACTGGATG
  61 AAAGGTCTTG ATGACTGTTT GCAGCAGTAT ATTAAGAACT TTGAGAGGGA GAAGATCAGT
 121 GGGGACCAGC TGCTGCGCAT TACACATCAG GAGCTAGAAG ATCTGGGGGT CAGCCGCATT
 181 GGCCATCAGG AACTGATCTT GGAAGCAGTT GACCTTCTGT GTGCATTGAA TTATGGCTTG
 241 GAAACAGAAA ATCTAAAAAC CCTTTCTCAC AAGTTGAATG CATCTGCCAA AAATCTGCAG
 301 AATTTTATAA CAGGAAGGAG AAGGAGTGGC CATTATGATG GGAGGACCAG CCGAAAATTG
 361 CCAAACGACT TTCTGACCTC AGTTGTGGAT CTGATTGGAG CAGCCAAGAG TCTGCTTGCC
 421 TGGTTGGACA GGTCACCATT TGCTGCTGTG ACAGACTATT CAGTTACAAG AAATAATGTC
 481 ATACAACTCT GCCTGGAGTT AACAACAATT GTGCAACAGG ATTGTACTGT ATATGAAACA
 541 GAGAATAAAA TTCTTCACGT GTGTAAAACT CTTTCTGGAG TCTGTGACCA CATCATATCC
 601 CTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTCACCTGG AAGTGATTCA ACTGGCAAAC
 661 ATTAAACCAA GCGAAGGGCT GGGTATGTAT ATTAAATCTA CATATGATGG CCTCCATGTA
 721 ATTACTGGAA CCACAGAAAA TTCACCTGCA GATCGGTGCA AGAAAATCCA TGCTGGCGAT
 781 GAAGTGATTC AAGTTAATCA TCAGACTGTG GTGGGGTGGC AGTTGAAAAA TTTGGTGAAT
 841 GCACTACGAG AGGACCCGAG TGGTGTTATC TTAACTTTGA AAAAGCGACC TCAGAGCATG
 901 CTTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA AGCCCCTTGC TCTGCAGCCT
 961 CTTATACCTA GAAGTCCCAC AAGCAGCGTT GCCACGCCTT CCAGCACCAT CAGTACACCC
1021 ACCAAAAGAG ACAGTTCTGC CCTCCAGGAT CTCTACATTC CCCTCCTCC TGCAGAACCA
1081 TATATTCCCA GGGATGAAAA AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATATGGTG
1141 GGCAAGCCAG TGCATAAGGG ATCTGAATCA CCAAATTCAT TTCTGGATCA GGAATATCGA
1201 AAGAGATTTA ATATTGTCGA GAAGATACT GTCTTATATT GCTATGAATA TGAAAAAGGA
1261 AGATCAAGTA GTCAAGGAG ACGAGAAAGC ACCCCAACTT ATGGCAAGCT ACGACCTATA
1321 TCTATGCCAG TGGAATATAA TTGGGTGGGG GACTATGAAG ATCCAAATAA GATGAAGAGA
1381 GATAGTAGAA GAGAAAACTC TCTACTTCGG TATATGAGCA ATGAAAAGAT TGCTCAAGAA
1441 GAATACATGT TTCAGAGAAA CAGCAAAAAG GACACAGGGA GAAGTCAAA AAAGAAGGGT
1501 GATAAGAGTA ATAGCCCAAC TCACTATTCA TTGCTACCTA GTTTACAAAT GGATGCACTG
1561 AGACAAGACA TCATGGGCAC TCCTGTGCCA GAGACCACAC TATACCATAC ATTTCAGCAG
1621 TCCTCACTGC AGCACAAATC AAAGAAGAAA AACAAAGGTC CTATAGCAGG CAAGAGCAAA
1681 AGACGAATTT CTTGCAAAGA TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAG
1741 AAAGATGCGA AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT
1801 GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT CATTAGCCTG
1861 CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA AATATGCATT CAAAGCCTGT
1921 CATCCTAAAA TCAAAAGCTT TTATTTTGCT GCTGAACATC TTGATGATAT GAACAGGTGG
1981 CTTAACAGAA TTAATATGCT GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA
2041 CAAGATTACT GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA
2101 GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG TTGCGCCAGT
2161 CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG AGACTTCTCA GTCTCAGTCT
2221 TCTCATGAGG AGTTTCGCCA GGAAGTAACT GGGAGCAGTG CAGTGTCTCC CATTCGCAAG
2281 ACAGCCAGTC AGCGCCGCTC CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC
2341 TTACACTATC TTCAGACTCT GCCCCTGGAG GATTCTGTCT TCTCTGACTC CGCGGCCATC
2401 TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT GCAGGATCAC
2461 TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG TGCTAAATGG AAATGGGGGC
2521 AAGCCTCGAA GTTTTACTCT GCCTCGAGAT AGCGGGTTCA ACCATTGCTG TCTGAATGCT
2581 CCAGTTAGTG CCTGTGACCC ACAGGATGAC GTGCAACCCC AGAGGTGGA GGAAGAGGAG
2641 GAGGAGGAGG AGGAGGAAGG GGAGGCAGCA GGGGAAAAACA TAGGAGAAAA AAGTGAAAGC
2701 AGAGAAGAAA AGTTAGGAGA CTCATTGCAA GATTTATACA GGGCACTGGA GCAGGCCAGT
2761 CTGTCACCAC TAGGAGAACA TCGTATTTCA ACCAAGATGG AATACAAGCT ATCATTTATA
2821 AAAAGATGTA ATGATCCTGT AATGAATGAA AAACTACACC GGCTGAGAAT TCTCAAAAGC
2881 ACTTTAAAGG CCAGAGAAGG GGAAGTAGCC ATTATCGATA AGTCCTAGA CAATCCAGAC
2941 TTGACATCTA AAGAATTCCA ACAATGGAAG CAGATGTACC TCGACCTTTT CTTGGATATC
3001 TGTCAAAATA CCACCTCAAA TGACCCACTG AGTATTTCTT CTGAAGTAGA TGTAATCACT
3061 TCCTCTCTAG CACACACTCA TTCATACATT GAAACGCATG TCTAA
```

Fig. 12: SEQ ID NO. 4: nucleotide sequence of human MAGUIN-2 coding sequence

Length: 2697 bp

```
   1    ATGGCTCTGA TAATGGAACC GGTGAGCAAA TGGTCTCCGA GTCAAGTAGT
  51    GGACTGGATG AAAGGTCTTG ATGACTGTTT GCAGCAGTAT ATTAAGAACT
 101    TTGAGAGGGA GAAGATCAGT GGGGACCAGC TGCTGCGCAT TACACATCAG
 151    GAGCTAGAAG ATCTGGGGGT CAGCCGCATT GGCCATCAGG AACTGATCTT
 201    GGAAGCAGTT GACCTTCTGT GTGCATTGAA TTATGGCTTG GAAACAGAAA
 251    ATCTAAAAAC CCTTTCTCAC AAGTTGAATG CATCTGCCAA AAATCTGCAG
 301    AATTTTATAA CAGGAAGGAG AAGGAGTGGC CATTATGATG GGAGGACCAG
 351    CCGAAAATTG CCAAACGACT TTCTGACCTC AGTTGTGGAT CTGATTGGAG
 401    CAGCCAAGAG TCTGCTTGCC TGGTTGGACA GGTCACCATT TGCTGCTGTG
 451    ACAGACTATT CAGTTACAAG AAATAATGTC ATACAACTCT GCCTGGAGTT
 501    AACAACAATT GTGCAACAGG ATTGTACTGT ATATGAAACA GAGAATAAAA
 551    TTCTTCACGT GTGTAAAACT CTTTCTGGAG TCTGTGACCA CATCATATCC
 601    CTGTCGTCAG ATCCTCTGGT TTCACAGTCT GCTCACCTGG AAGTGATTCA
 651    GCTGGCAAAC ATTAAACCAA GCGAAGGGCT GGGTATGTAT ATTAAATCTA
 701    CATATGATGG CCTCCATGTA ATTACTGGAA CCACAGAAAA TTCACCTGCA
 751    GATCGGTGCA AGAAAATCCA TGCTGGCGAT GAAGTGATTC AAGTTAATCA
 801    TCAGACTGTG GTGGGGTGGC AGTTGAAAAA TTTGGTGAAT GCACTACGAG
 851    AGGACCCGAG TGGTGTTATC TTAACTTTGA AAAAGCGACC TCAGAGCATG
 901    CTTACCTCAG CACCAGCTTT ACTGAAAAAT ATGAGATGGA AGCCCCTTGC
 951    TCTGCAGCCT CTTATACCTA GAAGTCCCAC AAGCAGCGTT GCCACGCCTT
1001    CCAGCACCAT CAGTACACCC ACCAAAAGAG ACAGTTCTGC CCTCCAGGAT
1051    CTCTACATTC CCCCTCCTCC TGCAGAACCA TATATTCCCA GGGATGAAAA
1101    AGGAAACCTT CCTTGTGAAG ACCTCAGAGG ACATATGGTG GGCAAGCCAG
1151    TGCATAAGGG ATCTGAATCA CCAAATTCAT TTCTGGATCA GGAATATCGA
1201    AAGAGATTTA ATATTGTCGA AGAAGATACT GTCTTATATT GCTATGAATA
1251    TGAAAAAGGA AGATCAAGTA GTCAAGGAAG ACGAGAAAGC ACCCCAACTT
1301    ATGGCAAGCT ACGACCTATA TCTATGCCAG TGGAATATAA TTGGGTGGGG
1351    GACTATGAAG ATCCAAATAA GATGAAGAGA GATAGTAGAA GAGAAAACTC
1401    TCTACTTCGG TATATGAGCA ATGAAAAGAT TGCTCAAGAA GAATACATGT
1451    TTCAGAGAAA CAGCAAAAAG GACACAGGGA AGAAGTCAAA AAAGAAGGGT
1501    GATAAGAGTA ATAGCCCAAC TCACTATTCA TTGCTACCTA GTTTACAAAT
1551    GGATGCACTG AGACAAGACA TCATGGGCAC TCCTGTGCCA GAGACCACAC
1601    TATACCATAC ATTTCAGCAG TCCTCACTGC AGCACAAATC AAAGAAGAAA
1651    AACAAAGGTC CTATAGCAGG CAAGAGCAAA AGACGAATTT CTTGCAAAGA
1701    TCTTGGCCGT GGTGACTGTG AGGGCTGGCT TTGGAAAAAG AAAGATGCGA
1751    AGAGTTACTT TTCACAGAAA TGGAAAAAAT ATTGGTTTGT CCTAAAGGAT
1801    GCATCCCTTT ATTGGTATAT TAATGAGGAG GATGAAAAAG CAGAAGGATT
1851    CATTAGCCTG CCTGAATTTA AAATTGATAG AGCCAGTGAA TGCCGCAAAA
1901    AATATGCATT CAAAGCCTGT CATCCTAAAA TCAAAAGCTT TTATTTTGCT
1951    GCTGAACATC TTGATGATAT GAACAGGTGG CTTAACAGAA TTAATATGCT
2001    GACTGCAGGA TATGCAGAAA GAGAGAGGAT TAAGCAGGAA CAAGATTACT
2051    GGAGTGAGAG TGACAAGGAA GAAGCAGATA CTCCATCAAC ACCAAAACAA
2101    GATAGCCCTC CACCCCCATA TGATACATAC CCACGACCTC CCTCGATGAG
2151    TTGCGCCAGT CCTTATGTGG AAGCAAAACA TAGCCGACTT TCCTCCACGG
2201    AGACTTCTCA GTCTCAGTCT TCTCATGAGG AGTTTCGCCA GGAAGTAACT
2251    GGGAGCAGTG CAGTGTCTCC CATTCGCAAG ACAGCCAGTC AGCGCCGCTC
2301    CTGGCAGGAT TTAATTGAGA CGCCACTGAC AAGTTCAGGC TTACACTATC
2351    TTCAGACTCT GCCCCTGGAG GATTCTGTCT CTCTGACTC CGCGGCCATC
2401    TCCCCAGAGC ACAGGCGGCA GTCTACCCTG CCAACTCAGA AATGCCACCT
2451    GCAGGATCAC TATGGGCCAT ACCCCTTAGC TGAGAGTGAG AGGATGCAAG
2501    TGCTAAATGG AAATGGGGGC AAGCCTCGAA GTTTTACTCT GCCTCGAGAT
2551    AGCGGGTTCA ACCATTGCTG TCTGAaTGCT CCAGTTAGTG CCTGTGACCC
2601    ACAGGATGAC GTGCAACCCC CAGAGGTGGA GGAAGAGGAG GAGGAGGAGG
2651    AGGAGGAAGG GGAGGCAGCA GGGGAAAACA TAGGAGAAAA AAGCTAA
```

Fig. 13: SEQ ID NO. 5: nucleotide sequence of human MAGUIN-1 cDNA

Length: 5749 bp

```
   1 CGGGCAGCTA GTCGTGCTCG GGGCTTCACT CCCGCGCGTG AGGCGAGCGG GCAAGTTGGC
  61 TGAGGGCGTG CGGCAGAGGC TGCTTCCCTC GGCGACGCGA CCCCTCAGCA ACTCAAGCTA
 121 TGAACTGAAG CTCCCTAGGG ACGGAGACCG GAGCGGAGCG GCGGAGGCAG CAGCAGCAGC
 181 AGCAGCAGCA GCAGCAGCAG CAGCCGCCGC CGCCGCCGCC TTAGCGGGAA CTGAGCAGAC
 241 CCGGCGCGGA GCCACGACTC CTGCACGTTT ACCTCCCTGT CGCCGTTCCT GCCGGCGGTT
 301 GGCTAAAAGA CGTTACAGCC GCGAGACCCG ACACACAAAA GCCGCTTTCT CCGCGCCGCC
 361 CGCCCAGGGA GGCTGCGGCC AGCAAGGGAC CCCACCTGAG AGCAGCTCGG GCTGCTGAGT
 421 TCGTTTTGTG TCTGAGCTCT GCGCTCTGCA CGGAACCGAC CCCGTACCCA TGGCTCTGAT
 481 AATGGAACCG GTGAGCAAAT GGTCTCCGAG TCAAGTAGTG GACTGGATGA AAGGTCTTGA
 541 TGACTGTTTG CAGCAGTATA TTAAGAACTT TGAGAGGGAG AAGATCAGTG GGGACCAGCT
 601 GCTGCGCATT ACACATCAGG AGCTAGAAGA TCTGGGGGTC AGCCGCATTG CCATCAGGA
 661 ACTGATCTTG GAAGCAGTTG ACCTTCTGTG TGCATTGAAT TATGGCTTGG AAACAGAAAA
 721 TCTAAAAACC CTTTCTCACA AGTTGAATGC ATCTGCCAAA AATCTGCAGA ATTTTATAAC
 781 AGGAAGGAGA AGGAGTGGCC ATTATGATGG GAGGACCAGC CGAAAATTGC CAAACGACTT
 841 TCTGACCTCA GTTGTGGATC TGATTGGAGC AGCCAAGAGT CTGCTTGCCT GGTTGGACAG
 901 GTCACCATTT GCTGCTGTGA CAGACTATTC AGTTACAAGA AATAATGTCA TACAACTCTG
 961 CCTGGAGTTA ACAACAATTG TGCAACAGGA TTGTACTGTA TATGAAACAG AGAATAAAAT
1021 TCTTCACGTG TGTAAAACTC TTTCTGGAGT CTGTGACCAC ATCATATCCC TGTCGTCAGA
1081 TCCTCTGGTT TCACAGTCTG CTCACCTGGA AGTGATTCAA CTGGCAAACA TTAAACCAAG
1141 CGAAGGGCTG GGTATGTATA TTAAATCTAC ATATGATGGC CTCCATGTAA TTACTGGAAC
1201 CACAGAAAAT TCACCTGCAG ATCGGTGCAA GAAAATCCAT GCTGGCGATG AAGTGATTCA
1261 AGTTAATCAT CAGACTGTGG TGGGGTGGCA GTTGAAAAAT TTGGTGAATG CACTACGAGA
1321 GGACCCGAGT GGTGTTATCT TAACTTTGAA AAAGCGACCT CAGAGCATGC TTACCTCAGC
1381 ACCAGCTTTA CTGAAAAATA TGAGATGGAA GCCCCTTGCT CTGCAGCCTC TTATACCTAG
1441 AAGTCCCACA AGCAGCGTTG CCACGCCTTC CAGCACCATC AGTACACCCA CCAAAAGAGA
1501 CAGTTCTGCC CTCCAGGATC TCTACATTCC CCCTCCTCCT GCAGAACCAT ATATTCCCAG
1561 GGATGAAAAA GGAAACCTTC CTTGTGAAGA CCTCAGAGGA CATATGGTGG GCAAGCCAGT
1621 GCATAAGGGA TCTGAATCAC CAAATTCATT TCTGGATCAG GAATATCGAA AGAGATTTAA
1681 TATTGTCGAA GAAGATACTG TCTTATATTG CTATGAATAT GAAAAAGGAA GATCAAGTAG
1741 TCAAGGAAGA CGAGAAAGCA CCCCAACTTA TGGCAAGCTA CGACCTATAT CTATGCCAGT
1801 GGAATATAAT TGGGTGGGGG ACTATGAAGA TCCAAATAAG ATGAAGAGAG ATAGTAGAAG
1861 AGAAAACTCT CTACTTCGGT ATATGAGCAA TGAAAAGATT GCTCAAGAAG AATACATGTT
1921 TCAGAGAAAC AGCAAAAAGG ACACAGGGAA GAAGTCAAAA AAGAAGGGTG ATAAGAGTAA
1981 TAGCCCAACT CACTATTCAT TGCTACCTAG TTTACAAATG GATGCACTGA GACAAGACAT
2041 CATGGGCACT CCTGTGCCAG AGACCACACT ATACCATACA TTTCAGCAGT CCTCACTGCA
2101 GCACAAATCA AAGAAGAAAA ACAAAGGTCC TATAGCAGGC AAGAGCAAAA GACGAATTTC
2161 TTGCAAAGAT CTTGGCCGTG GTGACTGTGA GGGCTGGCTT TGGAAAAAGA AAGATGCGAA
2221 GAGTTACTTT TCACAGAAAT GGAAAAAATA TTGGTTTGTC CTAAAGGATG CATCCCTTTA
2281 TTGGTATATT AATGAGGAGG ATGAAAAAGC AGAAGGATTC ATTAGCCTGC CTGAATTTAA
2341 AATTGATAGA GCCAGTGAAT GCCGCAAAAA ATATGCATTC AAAGCCTGTC ATCCTAAAAT
2401 CAAAAGCTTT TATTTTGCTG CTGAACATCT TGATGATATG AACAGGTGGC TTAACAGAAT
2461 TAATATGCTG ACTGCAGGAT ATGCAGAAAG AGAGAGGATT AAGCAGGAAC AAGATTACTG
2521 GAGTGAGAGT GACAAGGAAG AAGCAGATAC TCCATCAACA CCAAAACAAG ATAGCCCTCC
2581 ACCCCCATAT GATACATACC CACGACCTCC CTCGATGAGT TGCGCCAGTC CTTATGTGGA
2641 AGCAAAACAT AGCCGACTTT CCTCCACGGA GACTTCTCAG TCTCAGTCTT CTCATGAGGA
2701 GTTTCGCCAG GAAGTAACTG GGAGCAGTGC AGTGTCTCCC ATTCGCAAGA CAGCCAGTCA
2761 GCGCCGCTCC TGGCAGGATT TAATTGAGAC GCCACTGACA AGTTCAGGCT TACACTATCT
2821 TCAGACTCTG CCCCTGGAGG ATTCTGTCTT CTCTGACTCC GCGGCCATCT CCCCAGAGCA
```

```
2881 CAGGCGGCAG TCTACCCTGC CAACTCAGAA ATGCCACCTG CAGGATCACT ATGGGCCATA
2941 CCCCTTAGCT GAGAGTGAGA GGATGCAAGT GCTAAATGGA AATGGGGGCA AGCCTCGAAG

3001 TTTTACTCTG CCTCGAGATA GCGGGTTCAA CCATTGCTGT CTGAATGCTC CAGTTAGTGC
3061 CTGTGACCCA CAGGATGACG TGCAACCCCC AGAGGTGGAG GAAGAGGAGG AGGAGGAGGA
3121 GGAGGAAGGG GAGGCAGCAG GGGAAAACAT AGGAGAAAAA AGTGAAAGCA GAGAAGAAAA
3181 GTTAGGAGAC TCATTGCAAG ATTTATACAG GGCACTGGAG CAGGCCAGTC TGTCACCACT
3241 AGGAGAACAT CGTATTTCAA CCAAGATGGA ATACAAGCTA TCATTTATAA AAAGATGTAA
3301 TGATCCTGTA ATGAATGAAA AACTACACCG GCTGAGAATT CTCAAAAGCA CTTTAAAGGC
3361 CAGAGAAGGG GAAGTAGCCA TTATCGATAA AGTCCTAGAC AATCCAGACT TGACATCTAA
3421 AGAATTCCAA CAATGGAAGC AGATGTACCT CGACCTTTTC TTGGATATCT GTCAAAATAC
3481 CACCTCAAAT GACCCACTGA GTATTCTTC TGAAGTAGAT GTAATCACTT CCTCTCTAGC
3541 ACACACTCAT TCATACATTG AAACGCATGT CTAAATGTAT TCTGCCTTCA GACCATCTAG
3601 TACCTGCTGG TACTCTGAAC AAGTATATAA GGTAGTTTTT ATATCAATGT GTGGAACACT
3661 TGACAAGCTA TACTTTAATG TTACCAAACT ATATGAAACA AACCATATAT GGTCACAATA
3721 CCACTATCTT TAATGAGCAT TTGTATATTT TATATGCAAC AGTGCTCAGC TTATGTTTAC
3781 CATGTGCAAA ATCAACTGTC TTTAATGACT TAAAATTAAC TTTTGCAAAC AATTCTAAAT
3841 ACAGGTGGTC TTCAAGTAGT AAAACCACAA AAGGCAGTTT CTATCTATG GTCATCTTTT
3901 CTCCCTTTAA GTTAATTTTA TATAAACAAG ACTTCAAAAG TAAATCACAT TTTTTCAGGT
3961 GCAGACATCC TTGTGGGTGG GAAAGAATTT AAACCTTTTT TATATTTATT AAAATGTTCT
4021 AAGAATTTTC TTAAACATTG CACAAAGTTT AATGCTGTAG TTTTATTTTT GTGAAATGTA
4081 GATGCGCATA CAAGAGCTAA GCAAATAGA AGAGCATCGA CATAAGAAAA GTTCAGGTAT
4141 CTAATATTCG TCTTAATAGT CTATTAACTT GTGAAAGCTA AGTTAATGGA AATATTATTC
4201 CAAATCTATG AGAACACTTG GTGTATCAGG GCAAAGCTTT GTAAGATGTT TTTGTAACTA
4261 AGACCAAAAT TGAAGATAGA GCTGCTTTAT TTTCTTGGTT TAAATCTTCC TTTATTTTTG
4321 TAGTGATGAG ATGCTGATTG TGTACAGAAG AATTTGAGAG GGGATTTTTA AAAACTGACT
4381 TAACACACCC AGAAAGGCAG CTAACAGCTA TATATATATA TAAATTTCAG CCCAAACTCA
4441 TGTTTTTAAA CTCCAACTCT TAAAAGACAA CAAGGTATAA ACTGAAATGA ATCAACTTTC
4501 CACTTAGTTT CCAATTTTCC CCTAGTCCAC TAATTAAACT TAGGTAATTA TACTTCAGGT
4561 AGGGAAGTAC AATATGTTTA GTTTCAGGCT GATGTGTGTT ATAAAAAACA ACACTGAAAA
4621 ATAAAAATGT ACTTCCCTTC TAAGGAGCAA GCAGGTGATG GTCATTCAAA GAGATGTCAC
4681 ATTGAATTAT GAGAGAAACA ATTTAGAGGT TTTTTTCCTG GCTTCATGAA TTGTTCTATA
4741 GAGTGGATGA AGTCTAAGGA AAAGTCCTCT TCATATATTT CCATTTATAA GCGTCTTGTT
4801 TTTGAAAGTG ATCACAGCAT GAAAATGACT GTGCTGCTTT TTAGTGTCTG GCTGCATAAT
4861 GTACAAGTCA CAATTTGCTG TTTTTTTCAG GAGGAGAAAG GGAACCTCCT TTACTATTCT
4921 ATATCCTAAA ATCTACTTCT AATCAGCTTT ATACTGTTGC CTGTACAGCT CAGTGAATGT
4981 ACTTTCATCT TTAAGAGTTC AGATATATGC CAGTGAATAT TTTTGCTGTA GAGGAGAAAG
5041 TAAAAACTCC ACAGCGGGGA TCTTTTTCTT TGCTTTTGAA ACCACCATTG AATCACTATC
5101 GTTTTGCAGA CTTTGCACAA CTGTACAGGA GAGTGGCCTT TCTACAGCAC ATTTTCAGTA
5161 ATCCTATATT TAGTCAAAAT GGATGAGAAA TCATGTATTA ATGTTTGTAT GGAATTTTGG
5221 GTCCAGTGTA ATATTTTAT CATTTAAAAA GAACTCTATT TGTAAAAACA TTTATTTACT
5281 GCATGGATAT TGACGCACAT TAAATTTGTG GGATTTTGTA TATGTAAAAA AAAAAAAAAA
5341 AAAAAAAAC AAAAAACCTC TTGTCCTAAA ATGAAGTGTG CTTGTTAACA GGTGTTTAGA
5401 CTTATTGATG TTTACTAGAC CAAATGTGTA TGTTCACTTA AAAATATATG TACCTGATGG
5461 ATGTGTCATG TTTACAGTGG CCAGGTTGTG GCCTGTAAAC AGCAAGCAGT TGACGGGAAG
5521 ACTAGCTCTG TTGCTACTAA GCAGCTTTTA CTTTTGTAAA GTCAGCTCTG TTGTTTTAAA
5581 TGGTAAAAAT TAAACTAATG AATTTGACAA GACTCGTGGC TAGCCTAGCA TGAAAGAGAC
5641 CTTTTAACAC TATATAATAT CTGTACATTT TATTGCATTC GTTTCAAATC TAGGAGAGAG
5701 GCAGCACTGT AAACTGAAGT CAAATAAATT CAGCTCTTAA TGAATCCTT
```

Fig. 14: SEQ ID NO. 6: nucleotide sequence of human MAGUIN-2 cDNA

Length: 4350 bp

```
   1  GTGCTCGGGG CTTCACTCCC GCGCGTGAGG CGAGCGGGCA AGTTGGCTGA
  51  GGGCGTGCGG CAGAGGCTGC TTCCCTCGGC GACGCGACCC CTCAGCAACT
 101  CAAGCTATGA ACTGAAGCTC CCTAGGGACG GAGACCGGAG CGGAGCGGCG
 151  GAGGCAGCAG CAGCAGCAGC AGCAGCAGCA GCAGCAGCAG CCGCCGCCGC
 201  CGCCGCCTTA GCGGGAACTG AGCAGACCCG GCGCGGAGCC ACGACTCCTG
 251  CACGTTTACC TCCCTGTCGC CGTTCCTGCC GGCGGTTGGC TAAAAGACGT
 301  TACAGCCGCG AGACCCGACA CACAAAGCC GCTTTCTCCG CGCCGCCCGC
 351  CCAGGGAGGC TGCGGCCAGC AAGGGACCCC ACCTGAGAGC AGCTCGGGCT
 401  GCTGAGTTCG TTTTGTGTCT GAGCTCTGCG CTCTGCACGG AACCGACCCC
 451  GTACCCATGG CTCTGATAAT GGAACCGGTG AGCAAATGGT CTCCGAGTCA
 501  AGTAGTGGAC TGGATGAAAG GTCTTGATGA CTGTTTGCAG CAGTATATTA
 551  AGAACTTTGA GAGGGAGAAG ATCAGTGGGG ACCAGCTGCT GCGCATTACA
 601  CATCAGGAGC TAGAAGATCT GGGGGTCAGC CGCATTGGCC ATCAGGAACT
 651  GATCTTGGAA GCAGTTGACC TTCTGTGTGC ATTGAATTAT GGCTTGGAAA
 701  CAGAAAATCT AAAAACCCTT TCTCACAAGT TGAATGCATC TGCCAAAAAT
 751  CTGCAGAATT TTATAACAGG AAGGAGAAGG AGTGGCCATT ATGATGGGAG
 801  GACCAGCCGA AAATTGCCAA ACGACTTTCT GACCTCAGTT GTGGATCTGA
 851  TTGGAGCAGC CAAGAGTCTG CTTGCCTGGT TGGACAGGTC ACCATTTGCT
 901  GCTGTGACAG ACTATTCAGT TACAAGAAAT AATGTCATAC AACTCTGCCT
 951  GGAGTTAACA ACAATTGTGC AACAGGATTG TACTGTATAT GAAACAGAGA
1001  ATAAAATTCT TCACGTGTGT AAAACTCTTT CTGGAGTCTG TGACCACATC
1051  ATATCCCTGT CGTCAGATCC TCTGGTTTCA CAGTCTGCTC ACCTGGAAGT
1101  GATTCAGCTG GCAAACATTA AACCAAGCGA AGGGCTGGGT ATGTATATTA
1151  AATCTACATA TGATGGCCTC CATGTAATTA CTGGAACCAC AGAAAATTCA
1201  CCTGCAGATC GGTGCAAGAA AATCCATGCT GGCGATGAAG TGATTCAAGT
1251  TAATCATCAG ACTGTGGTGG GGTGGCAGTT GAAAAATTTG GTGAATGCAC
1301  TACGAGAGGA CCCGAGTGGT GTTATCTTAA CTTTGAAAAA GCGACCTCAG
1351  AGCATGCTTA CCTCAGCACC AGCTTTACTG AAAAATATGA GATGGAAGCC
1401  CCTTGCTCTG CAGCCTCTTA TACCTAGAAG TCCCACAAGC AGCGTTGCCA
1451  CGCCTTCCAG CACCATCAGT ACACCCACCA AAAGAGACAG TTCTGCCCTC
1501  CAGGATCTCT ACATTCCCCC TCCTCCTGCA GAACCATATA TTCCCAGGGA
1551  TGAAAAAGGA AACCTTCCTT GTGAAGACCT CAGAGGACAT ATGGTGGGCA
1601  AGCCAGTGCA TAAGGGATCT GAATCACCAA ATTCATTTCT GGATCAGGAA
1651  TATCGAAAGA GATTTAATAT TGTCGAAGAA GATACTGTCT TATATTGCTA
1701  TGAATATGAA AAAGGAAGAT CAAGTAGTCA AGGAAGACGA GAAAGCACCC
1751  CAACTTATGG CAAGCTACGA CCTATATCTA TGCCAGTGGA ATATAATTGG
1801  GTGGGGGACT ATGAAGATCC AAATAAGATG AAGAGAGATA GTAGAAGAGA
1851  AAACTCTCTA CTTCGGTATA TGAGCAATGA AAAGATTGCT CAAGAAGAAT
1901  ACATGTTTCA GAGAAACAGC AAAAAGGACA CAGGGAAGAA GTCAAAAAAG
1951  AAGGGTGATA AGAGTAATAG CCCAACTCAC TATTCATTGC TACCTAGTTT
2001  ACAAATGGAT GCACTGAGAC AAGACATCAT GGGCACTCCT GTGCCAGAGA
2051  CCACACTATA CCATACATTT CAGCAGTCCT CACTGCAGCA CAAATCAAAG
2101  AAGAAAACA AAGGTCCTAT AGCAGGCAAG AGCAAAGAC GAATTTCTTG
2151  CAAAGATCTT GGCCGTGGTG ACTGTGAGGG CTGGCTTTGG AAAAAGAAAG
2201  ATGCGAAGAG TTACTTTTCA CAGAAATGGA AAAAATATTG GTTTGTCCTA
2251  AAGGATGCAT CCCTTTATTG GTATATTAAT GAGGAGGATG AAAAAGCAGA
```

```
2301  AGGATTCATT AGCCTGCCTG AATTTAAAAT TGATAGAGCC AGTGAATGCC
2351  GCAAAAAATA TGCATTCAAA GCCTGTCATC CTAAAATCAA AAGCTTTTAT

2401  TTTGCTGCTG AACATCTTGA TGATATGAAC AGGTGGCTTA ACAGAATTAA
2451  TATGCTGACT GCAGGATATG CAGAAAGAGA GAGGATTAAG CAGGAACAAG
2501  ATTACTGGAG TGAGAGTGAC AAGGAAGAAG CAGATACTCC ATCAACACCA
2551  AAACAAGATA GCCCTCCACC CCCATATGAT ACATACCCAC GACCTCCCTC
2601  GATGAGTTGC GCCAGTCCTT ATGTGGAAGC AAAACATAGC CGACTTTCCT
2651  CCACGGAGAC TTCTCAGTCT CAGTCTTCTC ATGAGGAGTT TCGCCAGGAA
2701  GTAACTGGGA GCAGTGCAGT GTCTCCCATT CGCAAGACAG CCAGTCAGCG
2751  CCGCTCCTGG CAGGATTTAA TTGAGACGCC ACTGACAAGT TCAGGCTTAC
2801  ACTATCTTCA GACTCTGCCC CTGGAGGATT CTGTCTTCTC TGACTCCGCG
2851  GCCATCTCCC CAGAGCACAG GCGGCAGTCT ACCCTGCCAA CTCAGAAATG
2901  CCACCTGCAG GATCACTATG GGCCATACCC CTTAGCTGAG AGTGAGAGGA
2951  TGCAAGTGCT AAATGGAAAT GGGGGCAAGC CTCGAAGTTT TACTCTGCCT
3001  CGAGATAGCG GGTTCAACCA TTGCTGTCTG AaTGCTCCAG TTAGTGCCTG
3051  TGACCCACAG GATGACGTGC AACCCCCAGA GGTGGAGGAA GAGGAGGAGG
3101  AGGAGGAGGA GGAAGGGGAG GCAGCAGGGG AAAACATAGG AGAAAAAAGC
3151  TAATACACTG CGAGAGTTGG TAGAACCTCT CCATGCCAAA TCGGATCCAC
3201  TTCTGTTGGC ACTCAACCCA TTGGACTCAC AGATTGATAA GCTAATGTTT
3251  AGAGAATTTA GATCGGAGAG AGTCGGTACG GCGCAGACTC AACATCAACC
3301  TCTTGCAAGC AACTAAAATG GCCTCGTCCT TGCTGTTTAT AACAGAAAAC
3351  AGACTTGTAA AAAGCTTAGA TCATCAAGTG TTTTGGATTG GGGGCCTCCC
3401  AAAGGGATAT AAGAGGGGCA GGCCACTCTT AAGAAGAATG CGAGCTTTCT
3451  ACATTGGGAC TAGCATAAGA TCAAAGCCAA TCAAGATGGA GCACAGTAAC
3501  AGAAAACTGC GGTTTCTGTG GGAGAACAGA AGGGGAAAGG GTCTTAACTG
3551  GGAAAGGGCT CTGTGTGGTA ACACCTCAGT TGTGTTCTCC TGACACCAGG
3601  AAAAGAGAGG GATCAGCTTC AATAACTAGA AAATTCTGGC TGTTTAATGG
3651  ACTCTTTGGT GGCCTCTTTA AGGCAAAGCA GAGAAAGCAA ATTATGTATT
3701  AAGTGTATTT TGCATTTTTA AAACTTGACG TGCTGTATTG TACTAAATTA
3751  AGTGTAATCT ATTAAGGCAA GGTATACACA ATTTGCTTTG AAACTTACTA
3801  TGTTTATTCT ATTATAAAGT GTATTCAGGT GCAACACAGA GACTGCTTTC
3851  GGTGACATTA ATGAAGAAAA TTTCTCATGC CAGGCTTTAT TATAGAATCT
3901  TCAGCTAAAA TCCTAACTTT CTCCTTATTT CTTGGCACTT GTATACAAGT
3951  GGTGTTGCCT CTTAGGGCAG GCATGAGCTA TTCTTTTCTG TAAAATATTT
4001  TGAATCTATA GGCTGTGGGT TTCATTTTTG AAAAGTATTT TGTCTGGATG
4051  TCTTTCAAAC TAGCTTCAGA TATTATTTAA TACTATGTAA CTGGGTCCCC
4101  TATGGCTCAA TCAATATTGC TTATTTTTCT TCTGTAGTGG ATGTGAAATT
4151  TCCTTTAGTT GGATAAGATA CACTGTAATA ATTTTAATGC TAATTAATGA
4201  TATTTCATAC TGTGCAATGA ACAGATAATT TAACACTGTA TTTTGAAATG
4251  TTTTTTTCTT CCTGTCACCG CAGTGTGTGG TATTGCATAA TGTGAATACC
4301  TGTAAAAATA TAAATTACTT AAAAATAAAA ATATGACCAA TTGGTATCAG
```

Figure 15: SEQ ID NO. 7

Length: 50 bp

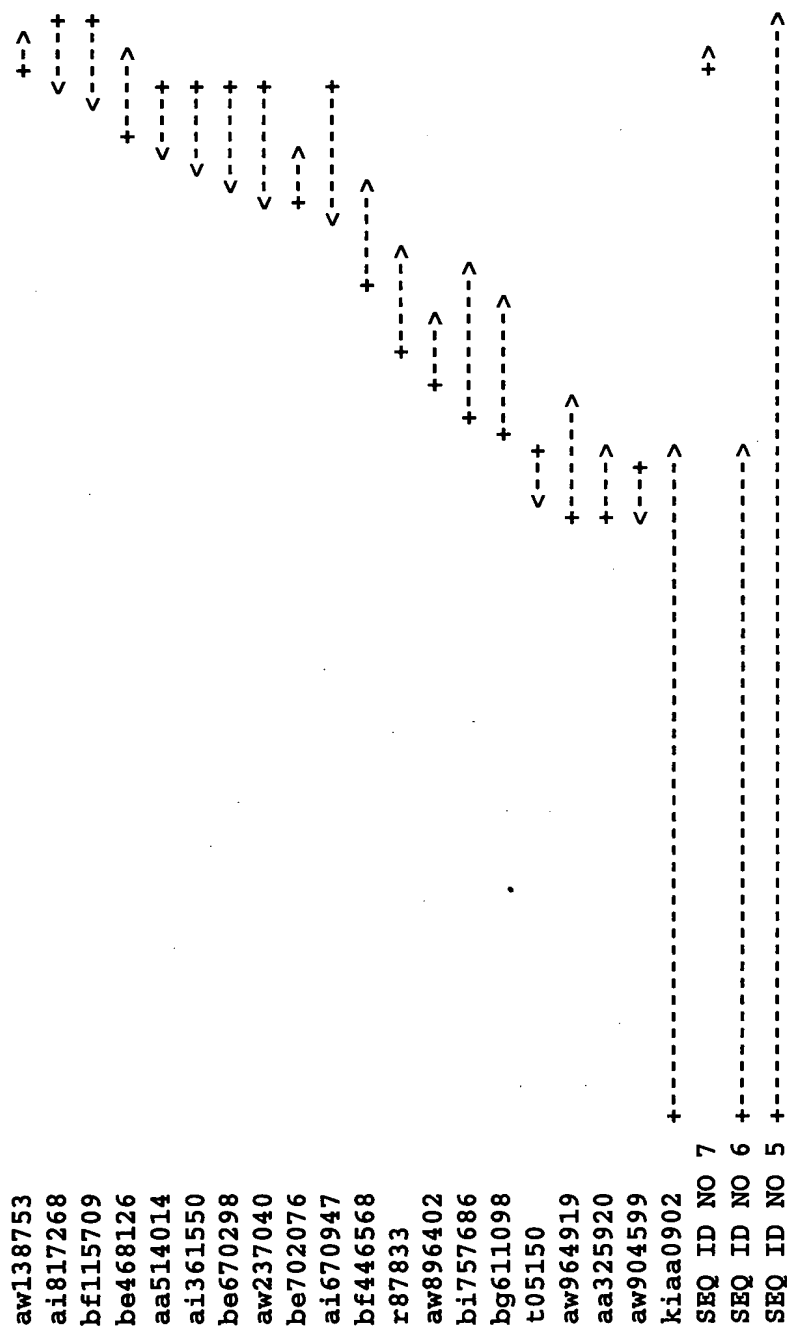1   GGAGAGAGGCAGCACTGTAAACTGAAGTCAAATAAATTCAGCTCTTAATG

Fig. 16: Alignment of SEQ ID NO. 7
with human MAGUIN-1 cDNA

Length: 50 bp

```
   1 GGAGAGAGGCAGCACTGTAAACTGAAGTCAAATAAATTCAGCTCTTAATG 50
     ||||||||||||||||||||||||||||||||||||||||||||||||||
5693 GGAGAGAGGCAGCACTGTAAACTGAAGTCAAATAAATTCAGCTCTTAATG 5742
```
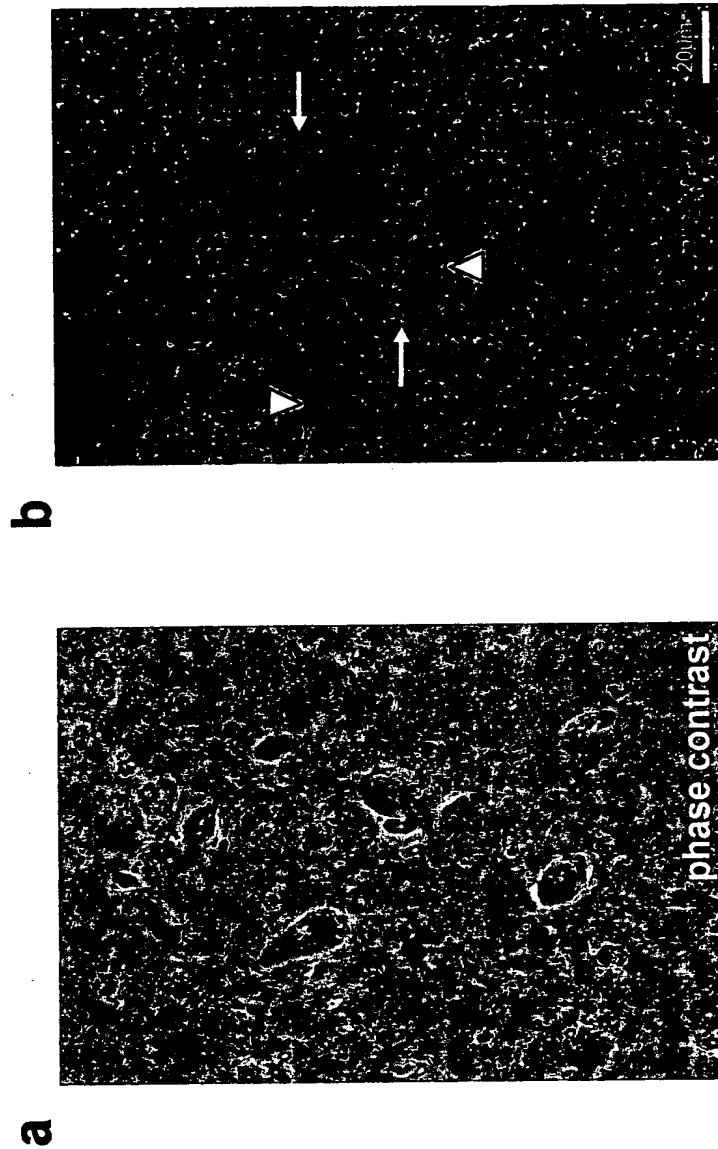
Fig. 17: Schematic alignment of SEQ ID NO. 5, SEQ ID NO. 6 and SEQ ID NO. 7 with Genome Database EST-cluster

Fig. 18: Images of the human cerebral cortex labeled with anti-Maguin-1 antiserum and with DAPI

10/508343

Table 1:

sample	Δ (fold) (frontal / temporal cortex)
patient P012	2.46
patient P016	2.78
patient P010	4.14
patient P011	2.20
patient P014	1.48
patient P017	1.42
patient P019	1.68
control C011	1.28
control C012	1.29
control C014	0.30
control C005	1.36
control C008	1.15

Table 2:

sample	Δ (fold) (frontal cortex / hippocampus)
patient P012	1.37
patient P016	3.07
patient P010	2.99
patient P011	2.28
patient P014	1.21
patient P019	1.48
control C005	1.74
control C008	0.39
control C004	0.87

Table 3:

sample	Δ (fold) (frontal / temporal cortex)
patient P012	2.68
patient P016	2.72
patient P010	11.73
patient P011	2.44
patient P014	1.77
patient P017	3.43
patient P019	4.02
control C011	1.42
control C012	1.22
control C014	0.30
control C005	0.92
control C008	0.81

Table 4:

sample	Δ (fold) (frontal cortex / hippocampus)
patient P012	1.57
patient P016	4.38
patient P010	9.08
patient P011	4.53
patient P014	0.72
patient P019	1.37
control C005	1.84
control C008	0.46
control C004	1.69